

EXHIBIT 7

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Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

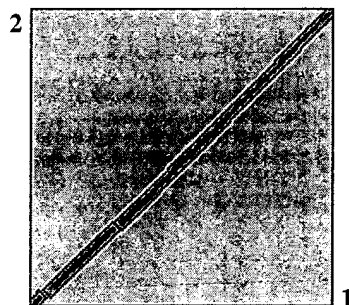
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.15 [Oct-15-2006]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0000** wordsize: **3** Filter ☐ View option: **Standard**
 Masking character option: **X for protein, n for nucleotide** Masking color option: **Black**
☐ Show CDS translation **Align**

Sequence 1: [gi|6678678|ref|NP_032519.1|leptin \[Mus musculus\]](#) >[gi|730219|sp|P41160|LEP_MOUSE](#) Leptin precursor (Obesity factor) >[gi|603288|gb|AAA64564.1|ob](#) >[gi|726297|gb|AAA64213.1|obesity protein](#) >[gi|26326917|dbj|BAC27202.1|unnamed protein product \[Mus musculus\]](#) >[gi|74216350|dbj|BAE25117.1|unnamed protein product \[Mus musculus\]](#) >[gi|115545388|gb|AAI25246.1|Leptin \[Mus musculus\]](#) >[gi|1092655|prf|2024338A](#) obeser gene
 Length = 167 (1 .. 167)

Sequence 2: [gi|2406650|gb|AAC60368.1|leptin \[Gallus gallus\]](#) >[gi|3024234|sp|O42164|LEP_CHICK](#) Leptin precursor (Obesity factor) >[gi|3435282|gb|AAC32380.1|leptin precursor \[Gallus gallus\]](#)
 Length = 163 (1 .. 163)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 301 bits (770), Expect = 1e-80
 Identities = 158/167 (94%), Positives = 159/167 (95%), Gaps = 4/167 (2%)

```

Query 1  MCWRPLCRFLWLWSYLSYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSAKQRTGL 60
          MCWRPLCR LWSYL YVQAVP Q QDDTKTLIKTIVTRINDISHT SVSAKQRTGL
Sbjct 1  MCWRPLCR---LWSYLVYVQAVPCQIFQDDTKTLIKTIVTRINDISHT-SVSAKQRTGL 56

Query 61  DFIPGLHPILSLSKMDQTLAVYQQVLTSLPSQNVLQIANDLENLRDLLHLLAFSKSCSLP 120
          DFIPGLHPILSLSKMDQTLAVYQQVLTSLPSQNVLQIANDLENLRDLLHLLAFSKSCSLP
Sbjct 57  DFIPGLHPILSLSKMDQTLAVYQQVLTSLPSQNVLQIANDLENLRDLLHLLAFSKSCSLP 116

Query 121 QTSGLQKPESLDGVLEASLYSTEVALSRLQGSQDILQQLDVSPEC 167
          QTSGLQKPESLDGVLEASLYSTEVALSRLQGSQDILQQLD+SPEC
Sbjct 117 QTSGLQKPESLDGVLEASLYSTEVALSRLQGSQDILQQLDISPEC 163
  
```

CPU time: 0.02 user secs.

0.01 sys. secs

0.03 total secs.

Lambda	K	H
0.319	0.133	0.387

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 312

Number of extensions: 119

Number of successful extensions: 3

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 167

Length of database: 1,565,033,500

Length adjustment: 124

Effective length of query: 43

Effective length of database: 1,565,033,376

Effective search space: 67296435168

Effective search space used: 67296435168

Neighboring words threshold: 9

X1: 16 (7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.8 bits)

S2: 73 (32.7 bits)